# *Cacna1f* Cas9-KO Strategy

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Design Date:2020-2-11

# Project Overview

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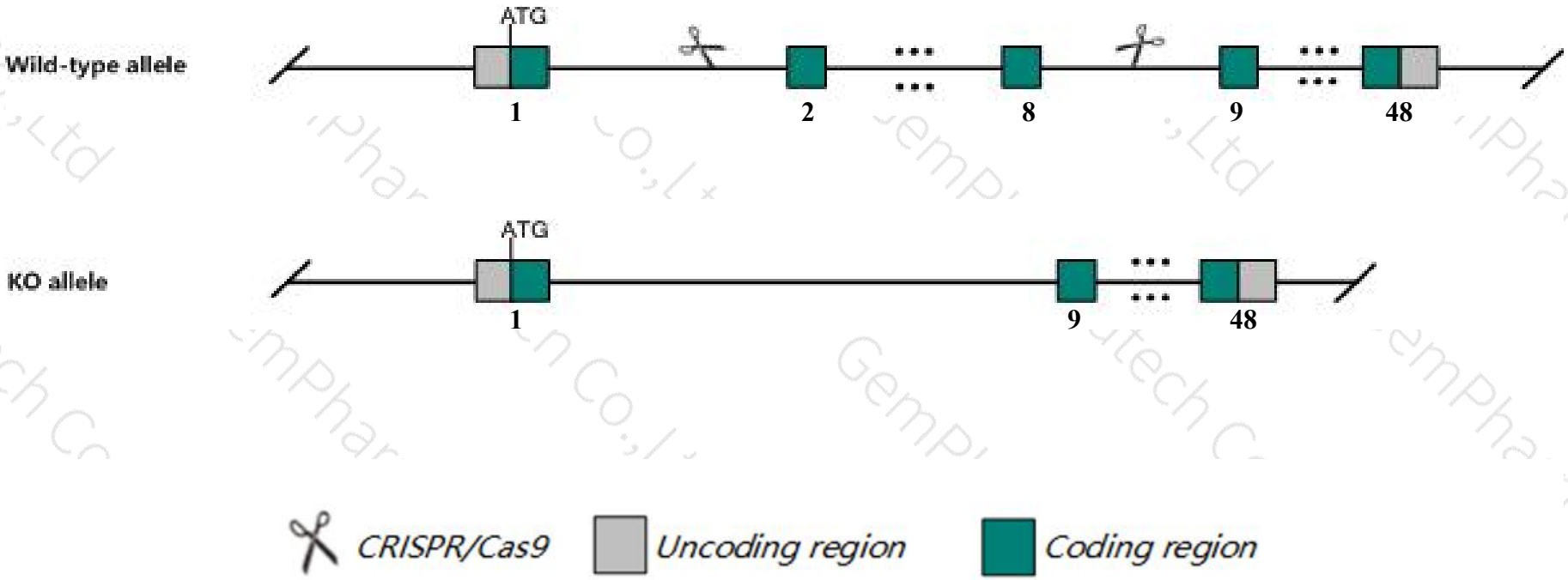
|---|---|
| **Project Name** | ***Cacna1f*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cacna1f* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Cacna1f* gene has 11 transcripts. According to the structure of *Cacna1f* gene, exon2-exon8 of *Cacna1f-202* (ENSMUST00000115726.8) transcript is recommended as the knockout region.The region contains 1093bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cacna1f* gene. The brief process is as follows: CRISPR/Cas9 syste

# Notice

- According to the existing MGI data,Homozygous or hemizygous mutation of this gene results in impaired eye electrophysiology, abnormal retinal neuronal layer, bipolar cell, and horizontal cell morphology, and impaired retinal synapse morphology.
- This strategy has no effect on transcripts *Cacna1f*-204,210.
- The knockout area is about 2.5kb away from the 5-terminal of Ccdc22 and Gm36995, which may affect its 5-terminal regulation after knockout.
- The *Cacna1f* gene is located on the ChrX. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases.Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

# Gene information（NCBI）

集萃药康 GemPharmatech

## Cacna1f calcium channel, voltage-dependent, alpha 1F subunit [ *Mus musculus* (house mouse) ]

Gene ID: 54652, updated on 27-Aug-2019

### Summary

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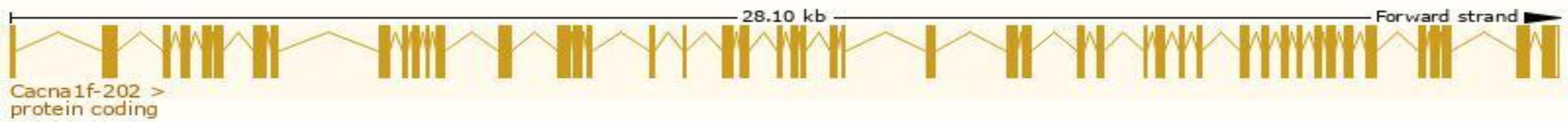
|---|---|
| **Official Symbol** | Cacna1f provided by MGI |
| **Official Full Name** | calcium channel, voltage-dependent, alpha 1F subunit provided by MGI |
| **Primary source** | MGI:MGI:1859639 |
| **See related** | Ensembl:ENSMUSG00000031142 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | nob2; Sfc17; nerg1; Cav1.4; A930034B14 |
| **Expression** | Low expression observed in reference dataset See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

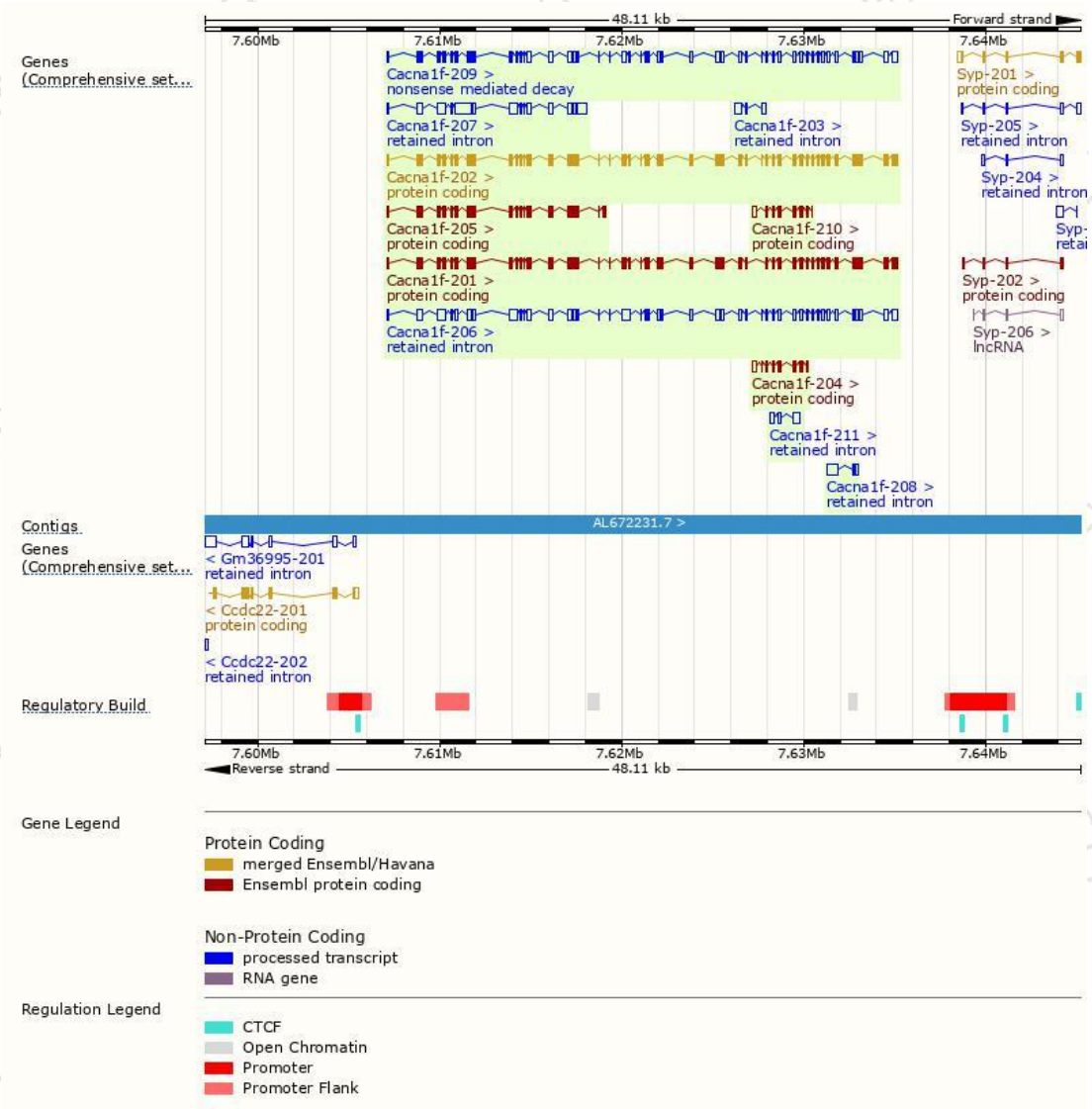
The gene has 11 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Cacna1f-202 | ENSMUST00000115726.8 | 6079 | 1984aa | Protein coding | CCDS40840 | Q7TNI3 | TSL:1 GENCODE basic APPRIS P2 |
| Cacna1f-201 | ENSMUST00000115725.8 | 6028 | 1977aa | Protein coding | - | B1AVA4 | TSL:5 GENCODE basic APPRIS ALT2 |
| Cacna1f-205 | ENSMUST00000133637.7 | 2559 | 844aa | Protein coding | - | Q8C8Q4 | CDS 3' incomplete TSL:1 |
| Cacna1f-210 | ENSMUST00000156047.1 | 921 | 247aa | Protein coding | - | B1AVA6 | CDS 3' incomplete TSL:5 |
| Cacna1f-204 | ENSMUST00000128628.7 | 869 | 229aa | Protein coding | - | B1AVA5 | CDS 3' incomplete TSL:3 |
| Cacna1f-209 | ENSMUST00000155090.7 | 6058 | 431aa | Nonsense mediated decay | - | S4R182 | TSL:5 |
| Cacna1f-206 | ENSMUST00000141634.7 | 6622 | No protein | Retained intron | - | - | TSL:2 |
| Cacna1f-207 | ENSMUST00000144522.7 | 3838 | No protein | Retained intron | - | - | TSL:2 |
| Cacna1f-208 | ENSMUST00000151208.1 | 820 | No protein | Retained intron | - | - | TSL:5 |
| Cacna1f-203 | ENSMUST00000123979.1 | 670 | No protein | Retained intron | - | - | TSL:3 |
| Cacna1f-211 | ENSMUST00000157000.1 | 642 | No protein | Retained intron | - | - | TSL:3 |

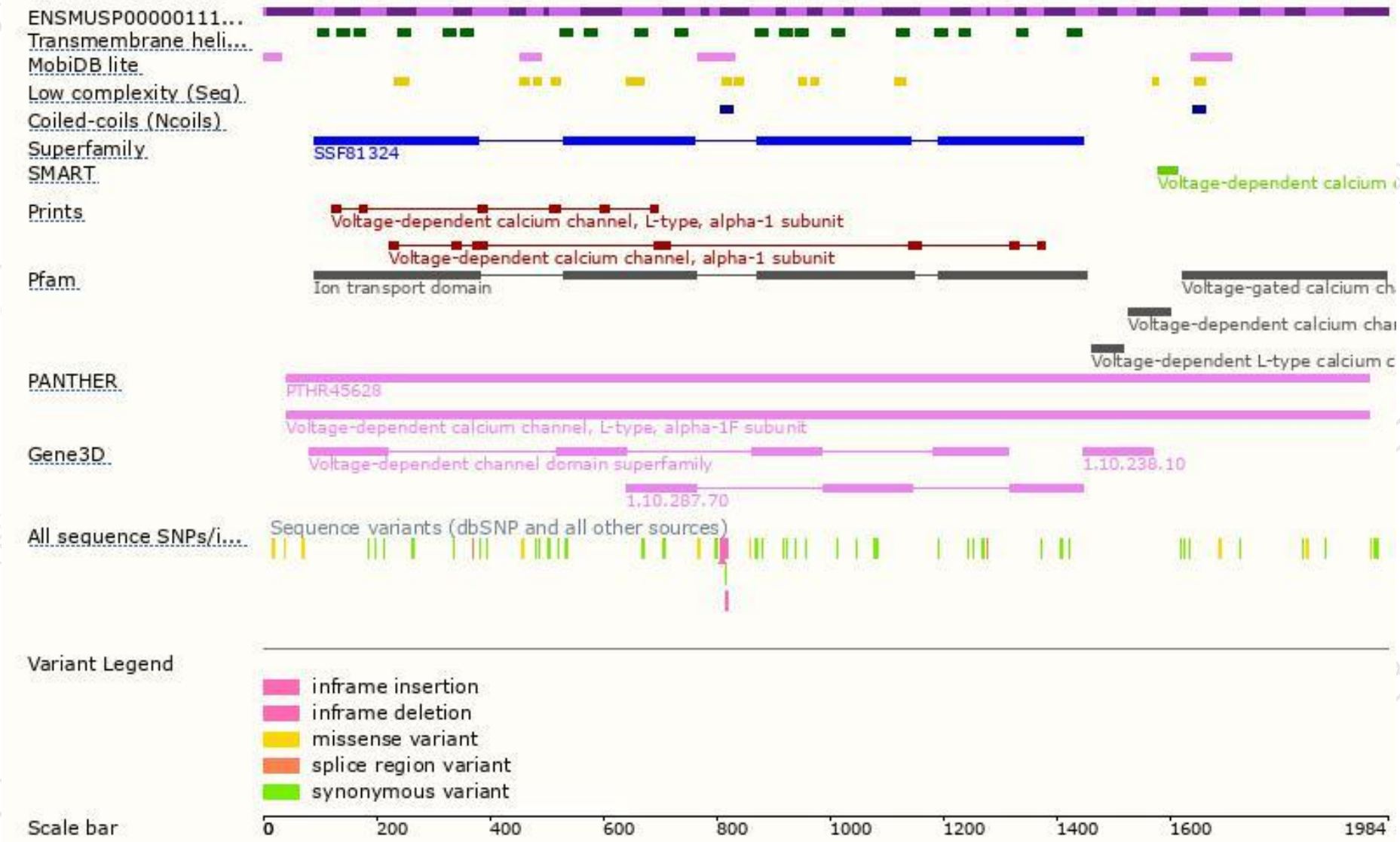
The strategy is based on the design of *Cacna1f-202* transcript,The transcription is shown below



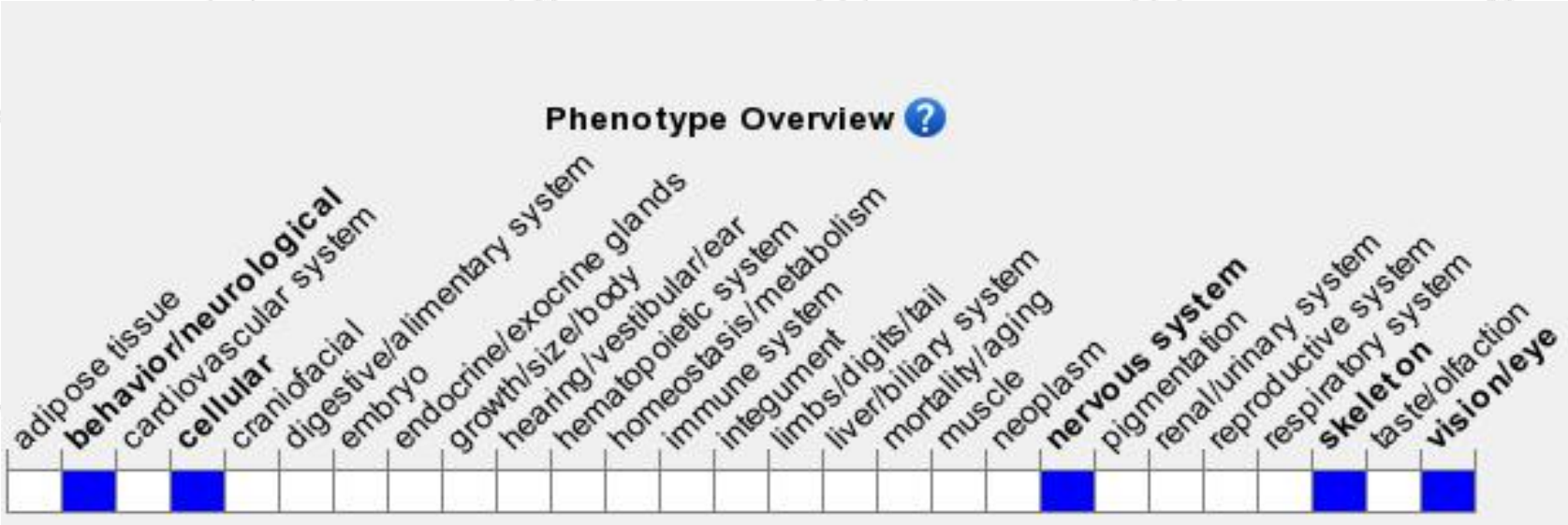
# Genomic location distribution



# Protein domain



# Mouse phenotype description(MGI )




*Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).*

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If you have any questions, you are welcome to inquire.

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